



Table IV: HLA Class I Standard Peptide Binding Affinity.

ALLELE	STANDARD PEPTIDE	SEQUENCE	SEQ ID NO:	STANDARD BINDING AFFINITY (nM)
A*0101	944.02	YLEPAIAKY	2109	25
A*0201	941.01	FLPSDYFPSV	2110	5.0
A*0202	941.01	FLPSDYFPSV	2111	4.3
A*0203	941.01	FLPSDYFPSV	2112	10
A*0205	941.01	FLPSDYFPSV	2113	4.3
A*0206	941.01	FLPSDYFPSV	2114	3.7
A*0207	941.01	FLPSDYFPSV	2115	23
A*6802	1072.34	YVIKVSARV	2116	8.0
A*0301	941.12	KVFPYALINK	2117	11
A*1101	940.06	AVDLYHFLK	2118	6.0
A*3101	941.12	KVFPYALINK	2119	18
A*3301	1083.02	STLPETYVRR	2120	29
A*6801	941.12	KVFPYALINK	2121	8.0
A*2402	979.02	AYIDNYNKF	2122	12
B*0702	1075.23	APRTLVL	2123	5.5
B*3501	1021.05	FPFKYAAAF	2124	7.2
B51	1021.05	FPFKYAAAF	2125	5.5
B*5301	1021.05	FPFKYAAAF	2126	9.3
B*5401	1021.05	FPFKYAAAF	2127	10

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Table V. HLA Class II Standard Peptide Binding Affinity.

Allele	Nomenclature	Standard Peptide	SEQ ID	Sequence	Binding Affinity (nM)
DRB1*0101	DR1	515.01	2128	PKYVKQNTLKLAT	5.0
DRB1*0301	DR3	829.02	2129	YKTIAFDEEARR	300
DRB1*0401	DR4w4	515.01	2130	PKYVKQNTLKLAT	45
DRB1*0404	DR4w14	717.01	2131	YARFQSQTTLKQKT	50
DRB1*0405	DR4w15	717.01	2132	YARFQSQTTLKQKT	38
DRB1*0701	DR7	553.01	2133	QYIKANSKFIGITE	25
DRB1*0802	DR8w2	553.01	2134	QYIKANSKFIGITE	49
DRB1*0803	DR8w3	553.01	2135	QYIKANSKFIGITE	1600
DRB1*0901	DR9	553.01	2136	QYIKANSKFIGITE	75
DRB1*1101	DR5w11	553.01	2137	QYIKANSKFIGITE	20
DRB1*1201	DR5w12	1200.05	2138	EALIHQLKINPYVLS	298
DRB1*1302	DR6w19	650.22	2139	QYIKANAKFIGITE	3.5
DRB1*1501	DR2w2β1	507.02	2140	GRTQDENPVVHFFK NIVTPRTPPP	9.1
DRB3*0101	DR52a	511	2141	NGQIGNDPNRDIL	470
DRB4*0101	DRw53	717.01	2142	YARFQSQTTLKQKT	58
DRB5*0101	DR2w2β2	553.01	2143	QYIKANSKFIGITE	20

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The "Nomenclature" column lists the allelic designations used in Tables XIX and XX.



SEQUENCE

Table XIX
CEA DR Super Motif Peptides with

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
IPWORLLLT	1962	RWCIPWORLLLTASL	1815	10	0.6100	0.0110	-0.0007	0.0150	0.0830	-0.0005		
WORLLLTAS	1963	CIPWORLLLTASLLT	1816	12								
LI.LTASLI.T	1964	WORLLLTASLLTFWN	1817	15								
LLTASLLTF	1965	ORELLTASLLTFWNP	1818	16	-0.0004				-0.0022			
LTASLI.TFW	1966	RI.LLTASLI.TFWNPP	1819	17								
TFWNPPTT	1967	ASLLTFWNPPTTAKL	1820	22								
FWNPPTTAK	1968	LI.TFWNPPTTAKLTI	1821	24								
WNPPTTAKL	1969	LTFWNPPTTAKLTIE	1822	25								
LTFTSPFN	1970	TAKI.TFTSPFNVAE	1823	33								
LVHNLPOH	1971	EVLLLVHNLPOHLFG	1824	50	2.5000	0.2300	0.0013	0.8900	0.8600	0.0340		
LVHNLPOHL	1972	VLI.LLVHNLPOHLFGY	1825	51								
YKGERVDGN	1973	YSWYKGERVDGNROI	1826	65								
IGVVGTO	1974	NROIIGVVGTOOAT	1827	76								
IGTOOATPG	1975	GYVIGTOOATPGPAY	1828	81								
YSGRFIYP	1976	GPAYSGRFIYPNAS	1829	92	0.6200	0.3800	0.0024	0.2700	0.0930	0.0029		
IYPNASLL	1977	GREIYPNASLLION	1830	97								
IYPNASLI	1978	REIYPNASLLIONII	1831	98								
LIIONII	1979	EIYPNASLLIONII	1832	99	0.3500	0.1600	-0.0007	0.1400	0.0390	-0.0005		
LIIONII	1980	NASLLIONIIIONDTG	1833	104	0.0011				-0.0022			
LIIONII	1981	ASLLIONIIIONDTG	1834	105								
LIIONII	1982	IONIIIONDTGFYTLH	1835	109	0.0720	0.0180	0.0250	0.0013	0.0260	0.0080		
LYTLHVKS	1983	DTGFYTLHVKS	1836	116								
LYTLHVKS	1984	TCFYTLHVKS	1837	117								
LYTLHVKS	1985	FYTLHVKS	1838	119								
LYTLHVKS	1986	LYTLHVKS	1839	121				0.1300				
LYTLHVKS	1987	LYTLHVKS	1840	122				0.0058				
LYTLHVKS	1988	LYTLHVKS	1841	126								
LYTLHVKS	1989	LYTLHVKS	1842	127								
LYTLHVKS	1990	LYTLHVKS	1843	137	0.0009				-0.0022			
LYTLHVKS	1991	LYTLHVKS	1844	141	0.0021				-0.0022			
LYTLHVKS	1992	LYTLHVKS	1845	146								
LYTLHVKS	1993	LYTLHVKS	1846	154								
LYTLHVKS	1994	LYTLHVKS	1847	176	8.4000	0.0830	0.0095	0.1300	5.6000	0.7000		
LYTLHVKS	1995	LYTLHVKS	1848	177	0.0230				0.0290			
LYTLHVKS	1996	LYTLHVKS	1849	197								
LYTLHVKS	1997	LYTLHVKS	1850	202								
LYTLHVKS	1998	LYTLHVKS	1851	218								
LYTLHVKS	1999	LYTLHVKS	1852	226								
LYTLHVKS	2000	LYTLHVKS	1853	231								
LYTLHVKS	2001	LYTLHVKS	1854	232								
LYTLHVKS	2002	LYTLHVKS	1855	239								
LYTLHVKS	2003	LYTLHVKS	1856	254								
LYTLHVKS	2004	LYTLHVKS	1857	268	0.0260	-0.0007	0.0033	0.0280	0.5600	0.0540		
LYTLHVKS	2005	LYTLHVKS	1858	281								
LYTLHVKS	2006	LYTLHVKS	1859	282								
LYTLHVKS	2007	LYTLHVKS	1860	283								
LYTLHVKS	2008	LYTLHVKS	1861	286								
LYTLHVKS	2009	LYTLHVKS	1862	288								
LYTLHVKS	2010	LYTLHVKS	1863	305	-0.0004				-0.0022			
LYTLHVKS	2011	LYTLHVKS	1864	310								
LYTLHVKS	2012	LYTLHVKS	1865	315				0.0042				
LYTLHVKS	2013	LYTLHVKS	1866	324					-0.0022			
LYTLHVKS	2014	LYTLHVKS	1867	332	-0.0004			0.0054	-0.0022			
LYTLHVKS	2015	LYTLHVKS	1868	337	0.0210				-0.0022			
LYTLHVKS	2016	LYTLHVKS	1869	380								
LYTLHVKS	2017	LYTLHVKS	1870	385								
LYTLHVKS	2018	LYTLHVKS	1871	392								

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SEQ-100001

Table XIX
CEA DR Super Motif Peptides with

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DR1	DR2wB1	DR2wB2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
LSVDHSDPV	2019	ONELSVDSHSDPVILN	1872	396				0.0820				
VDSHSDPVIL	2020	ELSVDSHSDPVILNVL	1873	398								
VILNVL YGP	2021	SDPVILNVL YGPDPP	1874	404								
YGPDDPTIS	2022	NVLYGPDPTISPSY	1875	410								
ISPSYTYR	2023	DPTISPSYTYRPGV	1876	417								
YTYRPGVN	2024	SPSYTYRPGVNLSL	1877	421								
YTRPGVNL	2025	SYTYRPGVNLSLSC	1878	423								
VNLSLSCH	2026	RPGVNLSLSCHAA	1879	428								
LSCHAA	2027	NLSLSCHAA	1880	432								
LIDGNIOOH	2028	YSLWIDGNIOOHTOE	1881	447								
IFISNITEK	2029	TOELFISNITEKNSG	1882	459								
FISNITEKN	2030	OELFISNITEKNLSGL	1883	460					0.0180			
ITEKNLSGLY	2031	ISNITEKNLSGLYTCO	1884	464								
LYTCOANNS	2032	NSGLYTCOANNSASG	1885	471								
VKTITVSAE	2033	RTTVKTTITVSAELPK	1886	488	0.0110	0.0250	0.0009	0.0010	0.0064		-0.0005	
VSAELPKPS	2034	TITVSAELPKPSISS	1887	493	-0.0004				-0.0022			
IPKPSISSN	2035	SAELPKPSISSNNK	1888	497								
WVGOSLPV	2036	YLVWVGOSLPVSPR	1889	532								
VNGOSLPVS	2037	LWVGOSLPVSPRL	1890	533								
LTLFNVTRN	2038	NRTLTLFNVTRNDAR	1891	553								
VTRNDARAY	2039	IFNVTRNDARAYVCG	1892	558								
IONSVSANR	2040	VCGIONSVSANRSDP	1893	570								
VSANRSDPV	2041	ONSVSANRSDPVTLID	1894	574								
VTLDVLYGP	2042	SDPVTLIDVLYGPDTP	1895	582					-0.0022			
LYGPDTPIL	2043	LDVLYGPDTPISPP	1896	587				0.0037				
YGPDPILIS	2044	DVLYGPDTPISPPD	1897	588								
ISPPDSSYL	2045	TPHISPPDSSYL.SGA	1898	595	-0.0004							
LSGANLNL	2046	SSYLSGANLNL.SCHS	1899	603								
LSCHSASNP	2047	NI.NLSCHSASNP.SPO	1900	610								
WRINGIPOO	2048	QYSWRINGIPOOHTO	1901	624								
IPOOHTOVL	2049	INGIPOOHTOVL.FIA	1902	629								
LFIKIPN	2050	TOVLFIKIPNNG	1903	637	0.0820				0.0037			
FIKIPN	2051	OVLFIKIPNNGT	1904	638	0.1200				0.0240			
IAKITPNN	2052	VLFIAKITPNNNGT	1905	639								
YACFVSNIA	2053	NGTYACFVSNLATGR	1906	650					0.0270			
VSNLATGRN	2054	ACFVSNLATGRNNSI	1907	653								
IVKSITVSA	2055	NNSIVKSITVSA	1908	654	0.0550	0.0029	-0.0007	0.1100	1.8000		0.0016	
VKSITVSA	2056	NSIVKSITVSA	1909	665	0.0640	0.0023	-0.0007	0.0750	1.8000		0.0012	
ITVSA	2057	NSIVKSITVSA	1910	666								
VSASGTS	2058	VKSITVSA	1911	669								
VSASGTS	2059	SITVSA	1912	671								
VSASGTS	2060	SPGLSAGATV	1913	680								
VSAGATVGI	2061	TVGIMIGV	1914	688								
IMIGV	2062	TAKLTIESTP	1915	33								
LTISTP	2063	YSWYKGERV	1916	65								
YKGERV	2064	NOSLPVSPRL	1917	182								
INLSCHAA	2065	GENINI.SCHAA	1918	252								
LPVSPRL	2066	GOSLPVSPRL	1919	538								

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Table XIX
CEA DR Super Motif Peptides with Binding

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IPWQRLLT	1962	RWCIPWQRLLTASL	1815	0.0110	0.0700	-0.0004		
WQRLTLTA	1963	CIPWQRLLTASLLT	1816					
LLLTASLLT	1964	WQRLLTASLLTFW	1817					
LLTASLLTF	1965	QRLLTASLLTFWNP	1818		-0.0013			
LTASLLTF	1966	RLLTASLLTFWNP	1819					
LTFWNPPT	1967	ASLLTFWNPPTAKL	1820					
FWNPPTTA	1968	LLTFWNPPTAKLTI	1821					
WNPPTTAK	1969	LTFWNPPTAKLTIE	1822					
LTISTFPN	1970	TAKLTISTFPNVAE	1823					
LVHNLPO	1971	EVLLLVHNLPOHLFG	1824	3.4000	0.4700	0.1200		
LVHNLPOH	1972	VLLLVHNLPOHLFGY	1825					
YKGERVDG	1973	YSWYKGERVDGNRQ	1826					
HGYVIGTQ	1974	NRQIGYVIGTQAT	1827					
IGTQOATPG	1975	GYVIGTQOATPGPAY	1828					
YSGREIYP	1976	GPA YSGREIYPNAS	1829					
IYPNASLL	1977	GREIYPNASLLIQN	1830	1.2000	0.5600	0.0083		
IYPNASLLIQ	1978	REIYPNASLLIQNI	1831					
LIQNIQ	1979	EIYPNASLLIQNII	1832	0.3100	0.1600	0.0029		
LIQNIQND	1980	NASLLIQNIQNDTG	1833		-0.0013			
IQNDTGFY	1981	ASLLIQNIQNDTGF	1834					
FYTLHVIKS	1982	IQNIQNDTGFYTLH	1835					
YTLHVIKSD	1983	DTGFYTLHVIKSDLV	1836					
LHVIKSDLV	1984	TGFYTLHVIKSDLVN	1837	0.0009	0.1100	0.0620		
VIKSDLVNE	1985	FYTLHVIKSDLVNEE	1838					
IKSDLVNEE	1986	TLHVIKSDLVNEEAT	1839					
LVNEEATG	1987	LHVIKSDLVNEEATG	1840					
VNEEATGQ	1988	KSDLVNEEATGQFRV	1841					
VYPPELKP	1989	SDLVNEEATGQFRVY	1842					
LKPSSISN	1990	QFRVYPELKPSSISS	1843					
ISSNSKPV	1991	YPELKPSSISSNSK	1844		-0.0013			
VEDKDAVA	1992	KPSSISSNSKPVEDK	1845		0.0033			
WVNNQSLP	1993	SKPVEDKDAVAFTCE	1846					
VNNQSLPV	1994	YLWVNNQSLPVSP	1847	1.5000	0.6000	0.0460		
LTLENVTR	1995	LWVNNQSLPVSPR	1848		0.0082			
VTRNDTAS	1996	NRTLFLFNVTRNDTA	1849					
VSARRSDS	1997	LFNVTRNDTASYKCE	1850					
VILNVLYGP	1998	ONPVSARRSDSVILN	1851					
LYGPDAPT	1999	SDSVILNVLYGPDAP	1852					
YGPDAPTIS	2000	LVNVLYGPDAPTISPL	1853					
ISPLNTSYR	2001	NVLVYGPDAPTISPLN	1854					
LSCHAAASN	2002	APTISPLNTSYRSGE	1855					
WFVNGTQ	2003	NLNLSCHAASNPPAQ	1856					
LFIPNITVN	2004	OYSWFVNGTFOQST	1857	0.0006	0.0270	0.0039		
FIPNITVNN	2005	TQELFIPNITVNNSG	1858					
IPNITVNS	2006	QELFIPNITVNNSGS	1859					
	2007	ELFIPNITVNNSGSY	1860					

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Table XIX CEA DR Super Motif Peptides with Binding

Seq ID Num

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
ITVNSGSY	2008	IPNITVNSGSYTCQ	1861					
VNNSGYT	2009	NITVNSGSYTCQAH	1862					
LNRTTVTI	2010	DTGLNRTTVTITIVY	1863		0.0088			
VTTITVYAE	2011	RTTIVTTITVYAEPPK	1864					
VYAEPPKP	2012	TITVYAEPPKPFITS	1865					
ITSNNSNPV	2013	KPFITSNNSNPVEDE	1866		-0.0013			
VEDEDAVA	2014	SNPVEDEDAVALTCE	1867					
LTLTSLVTR	2015	NRTLTLTSLVTRNDVG	1868		0.0021			
VTRNDVGP	2016	LLSVTRNDVGPYECG	1869					
VGPYECGI	2017	RNDVGPYECGIQNEL	1870					
IQNELSVDH	2018	ECGIQNELSVDHSDP	1871					
LSVDHSDP	2019	QNELSVDHSDPVILN	1872					
VDHSDPVIL	2020	ELSVDHSDPVILNVL	1873					
VILNLVYGP	2021	SDPVILNLVYGPDDP	1874					
YGPDDPTIS	2022	NVLVYGPDDPTISPSY	1875					
ISPSYTYR	2023	DPTISPSYTYRPGV	1876					
YTYRPGV	2024	SPSYTYRPGVNLSL	1877					
YYRPGVNL	2025	SYTYRPGVNLSLSC	1878					
VNLSLSCH	2026	RPGVNLSLSCHAAASN	1879					
LSCHAAASN	2027	NLSLSCHAAASNPPAQ	1880					
LIDGNIQOH	2028	YSLWIDGNIQOHTQE	1881					
LFISNITEK	2029	TOELFISNITEKNSG	1882		-0.0013			
FISNITEKN	2030	QELFISNITEKNSGL	1883					
ITEKNSGLY	2031	ISNITEKNSGLYTCQ	1884					
LYTCOANN	2032	NSGLYTCOANNAS	1885					
VKITVSAE	2033	RTTVKITVSAELPK	1886	0.0050	0.0790	-0.0004		
VSAELPKP	2034	TITVSAELPKPSISS	1887					
LPKPSISSN	2035	SAELPKPSISSNNSK	1888		-0.0013			
WVNGQSLP	2036	YLWVWVNGQSLPVSP	1889					
VNGQSLPV	2037	LWVWVNGQSLPVSPR	1890					
LTLFNVTR	2038	NRTLTLFNVTRNDAR	1891					
VTRNDARA	2039	LFNVTRNDARA YVC	1892					
IQNSVSAN	2040	VCGIQNSVSANRSDP	1893					
VSANRSDP	2041	QNSVSANRSDPVTLD	1894					
VTLDLVLY	2042	SDPVTLDVLVYGPDP	1895					
LYGPDTPII	2043	LDVLVYGPDPPIISP	1896		-0.0013			
YGPDPPIIS	2044	DVLVYGPDPPIISPPD	1897					
ISPPDSSYL	2045	TPHISPPDSSYLPGA	1898					
LSGANLNL	2046	SSYLPGANLNLSCHS	1899					
LSCHSASN	2047	NLNLCHSASNPSQP	1900					
WRINGIPQQ	2048	QYSWRINGIPQQHTQ	1901					
IPQQHTQVL	2049	INGIPQQHTQVLFLA	1902					
LFIKITPN	2050	TQVLFIAKITPNNG	1903		0.0038			
FIKITPN	2051	QVLFIAKITPNNGT	1904		0.0024			
IAKITPN	2052	VLFIKITPNNGTY	1905					
YACFVSNI	2053	NGTYACFVSNIATG	1906					

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Table XIX CEA DR Super Motif Peptides with Binding

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
FVSNLATG	2054	YACFVSNLATGRNN	1907		0.0070			
VSNLATGR	2055	ACFVSNLATGRNNSI	1908					
IVKSITVSA	2056	NNSIVKSITVSASGT	1909	0.0690	0.0370	0.0120		
VKSITVSAS	2057	NSIVKSITVSASGTS	1910	0.0460	0.0760	0.0170		
ITVSASGTS	2058	VKSITVSASGTSPGL	1911					
VSASGTSP	2059	SITVSASGTSPGLSA	1912					
LSAGATVGI	2060	SPGLSAGATVGIMIG	1913					
IMIGVLGV	2061	TVGIMIGVLGVALL	1914					
LTISTPFN	2062	TAKLTISTPFNVAE	1915					
YKGERVDG	2063	YSWYKGERVDGNRQ	1916					
LPVSPRLQ	2064	NQSLPVSPRLQLSNG	1917					
LNLSCHAA	2065	GENLNLSCHAAASNP	1918					
LPVSPRLQ	2066	GQSLPVSPRLQLSNG	1919					

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newed sum

[See ID no.]



CEA ID 000:

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Table XXa

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num
IQNDTGFT	2067	QNIQNIDTGFTLHV	1920
IKSDLVNEE	2068	LHVIKSDLVNEEATG	1921
LVNEEATGQ	2069	KSDLVNEEATGQFRV	1922
VNEEATGQF	2070	SDLVNEEATGQFRVY	1923
VYPELPKPS	2071	QFRVYPELPKPSISS	1924
FTCEPETQD	2072	AVAFCEPETQDATY	1925
YKCETQNPV	2073	TASYKCETQNPVSAR	1926
YGPDAPTIS	2074	NVLYGPDAPTISPLN	1927
VYAEPPKPF	2075	TITVYAEPPKPFITS	1928
VEDEDAVAL	2076	SNPVEDEDAVALTCE	1929
LTCEPEIQN	2077	AVALTCEPEIQNTTY	1930
IQNELSVDH	2078	ECGIQNELSVDHSDP	1931
LSVDHSDPV	2079	QNELSVDHSDPVILN	1932
YGPDDPTIS	2080	NVLYGPDPTISPSY	1933
VSAELPKPS	2081	TITVSAELPKPSISS	1934
FTCEPEAQN	2082	AVAFCEPEAQNTTY	1935
VTLDVLYGP	2083	SDPVTLDVLYGPDTP	1936
YGPDTPIIS	2084	DVLYGPDTPIIISPPD	1937

CEA DR 3a Motif Peptides with Binding

Position	DR1	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
110	0.0044	0.0105	-	0.3200	-0.0055	-	-	-0.0008
122	-	-	-	0.1300	-	-	-	-
126	-	-	-	0.0058	-	-	-	-
127	-	-	-	-	-	-	-	-
137	-	-	-	-	-	-	-	-
162	-	-	-	-	-	-	-	-
210	-	-	-	-	-	-	-	-
232	-	-	-	-	-	-	-	-
315	-	-	-	0.0042	-	-	-	-
332	-	-	-	0.0054	-	-	-	-
340	-	-	-	0.0039	-	-	-	-
392	-	-	-	-	0.0820	-	-	-
396	-	-	-	-	-	-	-	-
410	-	-	-	-	-	-	-	-
493	-	-	-	-	-	-	-	-
518	-	-	-	-	-	-	-	-
582	-	-	-	-	-	-	-	-
588	-	-	-	0.0037	-	-	-	-

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Section 1

CEA DR 3a Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Table XXa	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9	DRw53
IQNDTGFYT	2067	QNIQNDTGFYTLHV		1920	0.3600	-0.0017	-0.0009		
IKSDLVNEE	2068	LHVIKSDLVNEEATG		1921					
LVNEEATGQ	2069	KSDLVNEEATGQFRV		1922					
VNEEATGQF	2070	SDLVNEEATGQFRVY		1923					
VYPELPKPS	2071	QFRVYPELPKPSISS		1924					
FTCEPETQD	2072	AVAFCEPETQDATY		1925					
YKCEQNPV	2073	TASYKCETQNPVSAR		1926					
YGPDAPTIS	2074	NVLYGPDAPTISPLN		1927					
VYAEPPKPF	2075	TITVYAEPPKPFITS		1928					
VEDEDAVAL	2076	SNPVEDEDAVALTCE		1929					
LTCEPEIQN	2077	AVALTCEPEIQNTTY		1930					
IQNELSVDH	2078	ECGIQNELSVDHSDP		1931					
LSVDHSDPV	2079	QNELSVDHSDPVILN		1932					
YGPDDPTIS	2080	NVLYGPDPTISPSY		1933					
VSAELPKPS	2081	TITVSAELPKPSISS		1934					
FTCEPEAQN	2082	AVAFCEPEAQNTTY		1935					
VTLDVLYGP	2083	SDPVTLDVLYGPDTP		1936					
YGPDTPIIS	2084	DVLYGPDTPHISPPD		1937					

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CEA DR 3b Motif Peptides with Binding Data

Table XXb

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	Position	DRI	DR2w2B1	DR2w2B2	DR3	DR4w4	DR4w15	DR5w11	DR5w12
ATGQFRVVP	2085	NEEATGQFRVYP	1938	131				-0.0027				
LNTSYRSGE	2086	ISPLNTSYRSGENLN	1939	242				-0.0027				
YTCOAHNSD	2087	SGSYTCOAHNSDTGL	1940	294				-0.0027				
LPVSPRLQL	2088	NQSLPSPRLQLSND	1941	360				0.0071				
LSNDRTLT	2089	RQLSNDNRTLTLLS	1942	368		-0.0006	-0.0007	0.3200	-0.0055		-0.0008	
LSLSCHAS	2090	GVNLSLSCHASASNP	1943	430				0.0075				
LNLSCHAS	2091	GANLNLSCHASNPS	1944	608				-0.0027				
ASPETHLDM	2092	RLPASPEHLDMLRH	1945	34				-0.0027				
AHQVVRQVP	2093	VLIAHQVVRQVPQOR	1946	84				0.0290				
LIDTNRSA	2094	ALTIDTNRSRACHP	1947	180				0.0350				
IHNTHLCF	2095	LALIHNTLHCFVHT	1948	465		0.0590	0.0009	0.3100	-0.0055		0.0025	
LFRNPHQAL	2096	WDQLFRNPHQALLHT	1949	482		0.0015	-0.0007	0.9000	-0.0055		-0.0008	
VDLDDKQCP	2097	HSCVDLDDKQCPAEQ	1950	632				-0.0027				
YLEDVRLVH	2098	GMSTYLEVRLVHRDL	1951	832		-0.0006	0.0150	0.1800	-0.0055		-0.0008	
IDSECRPRF	2099	CWMIDSECRPRFREL	1952	958				0.4500				
AAPQHPPPP	2100	QGGAAAPQHPPPAFS	1953	1200				-0.0025				
AAISRKME	2101	EFQAAISRKMEVELVH	1954	104				0.0039				
LHHTLKIGG	2102	VKVLHHTLKIGGEPH	1955	284				-0.0025				
IGGEPHISY	2103	TLKIGGEPHISYPPL	1956	290				-0.0025				
AALSRKVAE	2104	EFQAAALSRKVAELVH	1957	104				0.0027				
ILGDPKLL	2105	EDSILGDPKLLTQH	1958	235		-0.0006	-0.0010	0.6700	-0.0055		-0.0008	
YKQSQHMT	2106	MAIYKQSQHMTVVVR	1959	160				-0.0025				
VEGNLRVEY	2107	LIRVEGNLRVEYLDD	1960	194				0.0930				
FTLQIRGRE	2108	GEYFTLQIRGRERFE	1961	325				0.0290				

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Table XXb
CEA DR 3b Motif Peptides with Binding Data

Core Sequence	Core SeqID Num	Exemplary Sequence	Exemplary SeqID Num	DR6w19	DR7	DR8w2	DR9
ATGQRVYP	2085	NEEATGQFRVYPPLP	1938				
LNTSYRSGE	2086	ISPLNTSYRSGENLN	1939				
YTCQAHNSD	2087	SGSYTCQAHNSDTGL	1940				
LPVSPRLQL	2088	NQSLPVSPRLQLSND	1941				
LSNDNRTL	2089	RLQLSNDNRTLTL	1942	0.0048	-0.0017	-0.0009	
LSLSCHAA	2090	GVNLSLSCHAA SNPP	1943				
LNLSCHAS	2091	GANLNLSCHASNPS	1944				
LNLSCHAS	2092	RLPASPEHLDMRLH	1945				
ASPETHLDM	2093	VLIAHQVYRQVPLQR	1946				
AHQVYRQVP	2094	ALTLDITNRSRACHP	1947				
LIDTNRSA	2095	LALIHNTLHLCFVHT	1948	0.7500	0.0200	0.0330	
IHNTHLCF	2096	WDQLFRNPHQALLHT	1949	0.0410	-0.0017	-0.0009	
LFRNPHQAL	2097	HSCVDLDDKGCPEAQ	1950				
VDLDDKGC	2098	GMSTYLEDVRLVHRDL	1951	(0.0001)	-0.0014	0.0028	
YLEDVRLVH	2099	CWMIDSECRPFREL	1952				
IDSECRPF	2100	OGGAAPQHPPPAFS	1953				
AAPQHPPP	2101	EFQAASIRKMMVELVH	1954				
AAISRKMMVE	2102	VKVLHHTLKIGGEPH	1955				
LHHTLKIGG	2103	TLKIGGEPHISYPPL	1956				
IGGEPHISY	2104	EFQAASIRKVAELVH	1957				
AALSRKVAE	2105	EDSILGDPKLLTOH	1958				
ILGDPKLL	2106	MAIYKQSQHMTVEVVR	1959				
YKQSQHMT	2107	LIRVEGNLRVEYLD	1960	0.0130	-0.0014	0.0029	
VEGNLRVEY	2108	GEYFTLQIRGRERE	1961				
FTLQIRGRE							

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pos 1, 2, 3, 4

Table XXII. Cross-reactive binding of CEA analog peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound
CEA.24	9	LLTFWNPPPT	2144	179	1720	67	755	-- ²	2
CEA.24M2V9	9	LMTFWNPPV	2145	4.5	782	7.7	34	3333	3
CEA.24V9	9	LLTFWNPPV	2146	16	307	26	56	952	4
CEA.78	9	QIIGYVIGT	2147	313	148	106	100	150	5
CEA.78L2V9	9	QLIGYVIGV	2158	9.4	5.9	2.3	21	2.3	5
CEA.233	10	VLYGPDAPTI	2149	128	606	270	804	--	2
CEA.233V10	10	VLYGPDAPTV	2150	26	430	16	206	952	4
CEA.411	10	VLYGPDDPTI	2151	294	358	476	7400	--	3
CEA.411V10	10	VLYGPDDPTV	2152	161	105	91	2467	--	3
CEA.569	9	YVCGIQNSV	2153	98	358	159	80	181	5
CEA.569L2	9	YLCGIQNSV	2154	50	24	12	31	3478	4
CEA.589	9	VLYGPDTPI	2155	200	878	53	638	--	2
CEA.589V9	9	VLYGPDTPV	2156	20	165	91	154	9756	4
CEA.605	9	YLSGANLNL	2157	28	165	2.4	804	--	3
CEA.605V9	9	YLSGANLNV	2158	73	13	13	80	1600	4
CEA.687	9	ATVGIMIGV	2159	36	8.8	20	11	0.80	5
CEA.687L2	9	ALVGIMIGV	2160	10	63	31	100	102	5
CEA.691	9	IMIGVLVGV	2161	69	62	13	106	89	5
CEA.691L2	9	ILIGVLVGV	2162	22	8.0	3.2	16	160	5

1) Wild-type peptides presented for reference purposes.

2) -- indicates binding affinity = 10,000nM.



TABLE XXII A A01 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0101 nM
52.0105	11	RVDGNRQIIGY	2163	CEA.72	294.1
52.0109	11	RSDSVILNVLY	2164	CEA.225	47.2
52.0113	11	HSDPVILNVLY	2165	CEA.403	25.8
52.0116	11	RSDPVTLDVLY	2166	CEA.581	7.8
57.0004	9	QQDTPGPAY	2167	CEA.87.D3	56.8
57.0007	9	AADNPPAQY	2168	CEA.261.D3	45.5
57.0008	9	ITDNNSGSY	2169	CEA.289.D3	96.2
57.001	9	VTDNDVGPY	2170	CEA.383.D3	4.1
57.0011	9	PTDSPSYTY	2171	CEA.418.D3	37.9
57.0012	9	TIDPSYTY	2172	CEA.419.D3	3.1
57.0013	9	AADNPPAQY	2173	CEA.439.D3	44.6
57.0014	9	ITDKNSGLY	2174	CEA.467.D3	11.9
57.0103	10	PTDSPLNTSY	2175	CEA.240.D3	266
57.0104	10	PTDSPSYTY	2176	CEA.418.D3	1.1
57.0105	10	HTASNPSPQY	2177	CEA.616.T2	131.6
57.0106	10	HSDSNPSPQY	2178	CEA.616.D3	44.6

↓
added



Table XXII B A03 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*0301 nM	A*1101 nM	A*3101 nM	A*3301 nM	A*6801 nM	A3 XRN
1371.01	10	TVSPLNTSYR	2179	CEA.241.V2	458.3	54.5	187.5	557.7	8.7	4
1371.02	10	TVSPLNTSYK	2180	CEA.241.V2K10	16.9	6.3	10588.2	-48333.3	7.3	3
1371.03	10	RVLTLSSVTR	2181	CEA.376.V2	343.8	222.2	11.3	6041.7	666.7	3
1371.04	10	RVLTLSSVTK	2182	CEA.376.V2K10	37.9	50	163.6	-72500	5714.3	3
1371.05	10	TVSPSYTYR	2183	CEA.419.V2	2340.4	3000	29	263.6	8.6	3
1371.06	10	TVSPSYTYK	2184	CEA.419.V2K10	68.8	42.9	3673.5	26363.6	6.7	3
1371.07	9	IVPSYTYR	2185	CEA.420.V2	91.7	13.3	25.7	58	2.6	5
1371.08	9	IVPSYTYK	2186	CEA.420.V2K9	17.2	54.5	720	4328.4	21.6	3
1371.09	10	RVLTLFNVTR	2187	CEA.554.V2	297.3	93.8	9	7631.6	42.1	4
1371.1	10	RVLTLFNVTK	2188	CEA.554.V42K10	20.8	31.6	233.8	41428.6	2352.9	3
1371.13	9	FVSNLATGK	2189	CEA.656.K9	1466.7	206.9	-36000	-72500	5.3	2

addd



Table XXII C A24 Analog Peptides

Peptide	AA	Sequence	SEQ ID NO:	Source	A*2401 nM
52.0033	8	IYPNASLL	2190	CEA.101	176.5
52.0038	8	SWFVNGTF	2191	CEA.270	480
52.0137	11	RWCIPWQRLLL	2192	CEA.10	151.9
52.0138	11	PWQRLLLTASL	2193	CEA.14	324.3
52.0141	11	FYTLHVIKSDL	2194	CEA.119	480
52.0142	11	TYLWWVNNQSL	2195	CEA.175	85.7
52.0144	11	TYLWWVNNQSL	2196	CEA.353	46.2
52.0145	11	SYTYRPGVNL	2197	CEA.423	218.2
52.0146	11	TYRPGVNLSL	2198	CEA.425	131.9
52.0147	11	TYLWWVNGQSL	2199	CEA.531	92.3
57.0036	9	RYCIPWQRF	2200	CEA.10.Y2F9	190.5
57.0037	9	IYPNASLLF	2201	CEA.101.F9	2.2
57.0038	9	LYWVNNQSF	2202	CEA.177.Y2F9	63.2
57.0039	9	LYGPDAPTF	2203	CEA.234.F9	63.2
57.0041	9	TYRPGVNF	2204	CEA.425.F9	52.2
57.0042	9	LYWVNGQSF	2205	CEA.533.Y2F9	15.8
57.0044	9	QYSWRINGF	2206	CEA.624.F9	109.1
57.0045	9	TYACFVSNF	2207	CEA.652.F9	8.6
57.0072	10	RYCIPWQRLF	2208	CEA.10.Y2F10	26.1
57.0073	10	FYNPPTTAKF	2209	CEA.27.Y2F10	181.8
57.0074	10	VYPELPKPSF	2210	CEA.140.F10	106.2
57.0075	10	TYQQSTQELF	2211	CEA.276.Y2	307.7
57.0076	10	VYAEPKPF	2212	CEA.318.F10	26.7
57.0077	10	YYRPGVNLSF	2213	CEA.426.F10	10
57.0078	10	QYSWLIDGNF	2214	CEA.446.F10	60
57.0079	10	SYLSGANLNF	2215	CEA.604.F10	10

↓
add



Table XXIII. Immunogenicity of A2 supermotif-bearing peptides

Peptide	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Bound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
CEA.78	9	QILGYVIGT	2216	313	148	106	100	151	5		0/3	
CEA.354	10	YLWWVNNQSI	2217	26	108	26	487	333	5		1/2	0/1
CEA.569	9	YVCGIQNSV	2218	98	358	159	80	182	5		1/2	0/1
CEA.605	9	YLSGANLNL	2219	28	165	2	804	-- ²	3		2/2	1/2
CEA.687	9	ATVGIMIGV	2220	36	9	20	11	1	5		1/1	1/1
CEA.691	9	IMIGVLVGV	2221	69	62	13	106	89	5		8/8	4/7
CEA.24	9	LLTFWNPPT	2222	179	1720	67	755	-- ²	2		0/1	0/1
CEA.24V9	9	LLTFWNPV	2223	16	307	26	56	952	4	1/1		1/1
CEA.233	10	VLYGPDPTI	2224	128	606	270	804	--	2		2/4	0/3
CEA.233V10	10	VLYGPDPTV	2225	26	430	16	206	952	4	3/4	2/2	1/4
CEA.589	9	VLYGPDPTI	2226	200	878	53	638	--	2		1/1	0/1
CEA.589V9	9	VLYGPDTPV	2227	20	165	91	154	9756	4	2/2	2/2	0/2
CEA.605	9	YLSGANLNL	2228	28	165	2.4	804	--	3		2/2	1/2
CEA.605V9	9	YLSGANLNV	2229	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

added



Table XXIV. MHC-peptide binding assays: cell lines and radiolabeled ligands.

A. Class I binding assays				Radiolabeled peptide		SEQ ID NO:
Species	Antigen	Allele	Cell line	Source	Sequence	
Human	A1	A*0101	Steinlin	Hu. J chain 102-110	YTAVVPLVY	2230
	A2	A*0201	JY	HBVc 18-27 F6->Y	FLPSDYFPPSV	2231
	A2	A*0202	P815 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPPSV	2232
	A2	A*0203	FUN	HBVc 18-27 F6->Y	FLPSDYFPPSV	2233
	A2	A*0206	CLA	HBVc 18-27 F6->Y	FLPSDYFPPSV	2234
	A2	A*0207	721.221 (transfected)	HBVc 18-27 F6->Y	FLPSDYFPPSV	2235
	A3		GM3107	non-natural (A3CON1)	KVFPYALINK	2236
	A11		BVR	non-natural (A3CON1)	KVFPYALINK	2237
	A24	A*2402	KAS116	non-natural (A24CON1)	AYIDNKNKF	2238
	A31	A*3101	SPACH	non-natural (A3CON1)	KVFPYALINK	2239
	A33	A*3301	LWAGS	non-natural (A3CON1)	KVFPYALINK	2240
	A28/68	A*6801	CIR	HBVc 141-151 T7->Y	STLPETYVVR	2241
	A28/68	A*6802	AMAI	HBV pol 646-654 C4->A	FTQAGYPAL	2242
	B7	B*0702	GM3107	A2 signal seq. 5-13 (L7->Y)	APRTLVL	2243
	B8	B*0801	Steinlin	HIV gp 586-593 Y1->F, Q5->Y	FLKDYQLL	2244
	B27	B*2705	LG2	R 60s	FRYNGLIHR	2245
	B35	B*3501	CIR, BVR	non-natural (B35CON2)	FPFKYAAAF	2246
	B35	B*3502	TISI	non-natural (B35CON2)	FPFKYAAAF	2247
	B35	B*3503	EHM	non-natural (B35CON2)	FPFKYAAAF	2248
	B44	B*4403	PITOUT	EF-1 G6->Y	AEMGKYSFY	2249
	B51		KAS116	non-natural (B35CON2)	FPFKYAAAF	2250
	B53	B*5301	AMAI	non-natural (B35CON2)	FPFKYAAAF	2251
	B54	B*5401	KT3	non-natural (B35CON2)	FPFKYAAAF	2252
	Cw4	Cw*0401	CIR	non-natural (C4CON1)	QYDDAVYKL	2253
	Cw6	Cw*0602	721.221 transfected	non-natural (C6CON1)	YRHDGNNVL	2254
	Cw7	Cw*0702	721.221 transfected	non-natural (C6CON1)	YRHDGNNVL	2255
Mouse	D ^b		EL4	Adenovirus E1A P7->Y	SGFSNTYPEI	2256
	K ^b		EL4	VSV NP 52-59	RGYVFGQL	2257
	D ^d		P815	HIV-III ENV G4->Y	RGPYRAFTI	2258
	K ^d		P815	non-natural (KdCON1)	KFNPMKTYI	2259
	L ^d		P815	HBV's 28-39	IPQSLDSYWTSL	2260



B. Class II binding assays

Species			Radiolabeled peptide		SEQ ID NO.
Antigen	Allele	Cell line	Source	Sequence	
Human	DR1	DRB1*0101	LG2	YPKYVKQNTLKLAT	2261
	DR2	DRB1*1501	L466.1	VVHFFKNIIVTPRTPPY	2262
	DR2	DRB1*1601	L242.5	YAAFAAAKTAATAFA	2263
	DR3	DRB1*0301	MAT	YKTIADFEEARR	2264
	DR4w4	DRB1*0401	Preiss	YARFQSQTTLKQKT	2265
	DR4w10	DRB1*0402	YAR	YARFQQTTLKAAA	2266
	DR4w14	DRB1*0404	BIN 40	YARFQSQTTLKQKT	2267
	DR4w15	DRB1*0405	KT3	YARFQSQTTLKQKT	2268
	DR7	DRB1*0701	Pitout	QYIKANSKFIGITE	2269
	DR8	DRB1*0802	OLL	QYIKANSKFIGITE	2270
	DR8	DRB1*0803	LUY	QYIKANSKFIGITE	2271
	DR9	DRB1*0901	HID	QYIKANSKFIGITE	2272
	DR11	DRB1*1101	Sweig	QYIKANSKFIGITE	2273
	DR12	DRB1*1201	Herluf	EALIHQLKINPYVLS	2274
	DR13	DRB1*1302	H0301	QYIKANAKFIGITE	2275
	DR51	DRB5*0101	GM3107 or L416.3	QYIKANAKFIGITE	2276
	DR51	DRB5*0201	L255.1	PKYVKQNTLKLAT	2277
	DR52	DRB3*0101	MAT	NGQIGNDPNRDIL	2278
	DR53	DRB4*0101	L257.6	YARFQSQTTLKQKT	2279
	DQ3.1	QA1*0301/DQB1*0301	PF	YAHAAHAAHAAHAAHAA	2280
Mouse	IA ^b		DB27.4	YAHAAHAAHAAHAAHAA	2281
	IA ^d		A20	YAHAAHAAHAAHAAHAA	2282
	IA ^k		CH-12	YNTDGSTDYGILQINSR	2283
	IA ^s		LS102.9	YAHAAHAAHAAHAAHAA	2284
	IA ^u		91.7	YAHAAHAAHAAHAAHAA	2285
	IE ^d		A20	YLEDARRKKAIYEKKK	2286
	IE ^k		CH-12	YLEDARRKKAIYEKKK	2287

add



Table XXVI. Crossbinding data of A2 supermotif peptides.

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound
CEA.24	9	LLTFWNPPT	2288	179	1720	67	755	--	2
CEA.78	9	QIIGYVIGT	2289	313	148	106	100	150	5
CEA.233	10	VLYGPDAPTI	2290	128	606	270	804	--	2
CEA.354	10	YLWWVNNQSL	2291	26	108	26	487	67	5
CEA.411	10	VLYGPDPTI	2292	294	358	476	7400	--	3
CEA.432	9	NLSLSCHAA	2293	455	2867	1449	18500	--	1
CEA.532	10	YLWWVNGQSL	2294	33	331	21	2056	286	4
CEA.569	9	YVCGIQNSV	2295	98	358	159	80	181	5
CEA.589	9	VLYGPDPTI	2296	200	878	53	638	--	2
CEA.605	9	YLSGANLNL	2297	28	165	2.4	804	--	3
CEA.687	9	ATVGIMIGV	2298	36	8.8	20	11	0.80	5
CEA.690	10	GIMIGVLGV	2299	64	205	31	142	500	5
CEA.691	9	IMIGVLGV	2300	69	62	13	106	89	5
CEA.691	10	IMIGVLGVA	2301	227	68	44	726	1509	3

-- indicates binding affinity = 10,000nM.

added



Table XXVII. Immunogenicity of A2 supermotif peptides

Source	AA	Sequence	SEQ ID NO:	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Wild-type I	CTL Tumor
CEA.78	9	QIIGYVIGT	2302	313	148	106	100	151	5	0/3	
CEA.354	10	YLWWVNNQSL	2303	26	108	26	487	333	5	1/2	0/1
CEA.569	9	YVCGIQNSV	2304	98	358	159	80	182	5	1/2	0/1
CEA.605	9	YLSGANLNL	2305	28	165	2.4	804	-- ²	3	2/2	1/2
CEA.687	9	ATVGIMIGV	2306	36	8.8	20	11	0.80	5	1/1	1/1
CEA.691	9	IMIGVLGV	2307	69	62	13	106	89	5	8/8	4/7

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

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Table XXVIII. Immunogenicity A2 supermotif analog peptides

Source	AA	Sequence	SEQ ID NO.	A*0201 nM	A*0202 nM	A*0203 nM	A*0206 nM	A*6802 nM	No. A2 Alleles Crossbound	CTL Peptide ¹	CTL Wild-type	CTL Tumor
CEA.24	9	LLTFWNPPT	2308	179	1720	67	755	-- ²	2		0/1	0/1
CEA.24V9	9	LLTFWNPV	2309	16	307	26	56	952	4	1/1		1/1
CEA.233	10	VLYGPDAPT	2310	128	606	270	804	--	2		2/4	0/3
CEA.233V10	10	VLYGPDAPT	2311	26	430	16	206	952	4	3/4	2/2	1/4
CEA.589	9	VLYGPDTP	2312	200	878	53	638	--	2		1/1	0/1
CEA.589V9	9	VLYGPDTP	2313	20	165	91	154	9756	4	2/2	2/2	0/2
CEA.605	9	YLSGANLNL	2314	28	165	2.4	804	--	3		2/2	1/2
CEA.605V9	9	YLSGANLNV	2315	73	13	13	80	1600	4	4/4	3/4	1/4

1) Number of donors yielding a positive response/total tested.

2) -- indicates binding affinity = 10,000nM.

added



Table XXIX. DR supertype primary binding

Peptide	DR147 Algo Sum	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR147 Cross- reactivity
39.0217	2	RWCIPWQRLLLTASL	2316	CEA.10	8.2	542	357	3
39.0218	3	QRLLLTASLLTFWNP	2317	CEA.16	--	--	--	0
39.0219	2	EVLLLVHNLQPQLFG	2318	CEA.50	2.0	52	53	3
39.0220	3	GREIYPNASLLIQN	2319	CEA.97	8.1	484	45	3
39.0221	2	EIIYPNASLLIQNII	2320	CEA.99	14	1154	156	2
39.0222	2	NASLLIQNIIQNDTG	2321	CEA.104	4546	--	--	0
39.0223	3	DTGFYTLHVIKSDLV	2322	CEA.116	69	1731	227	2
39.0224	2	YPELPKPSISSNNSK	2323	CEA.141	5556	--	--	0
39.0225	2	KPSISSNNSKPVEDK	2324	CEA.146	2381	--	7576	0
39.0226	3	YLWVWNNQSLPVSPR	2325	CEA.176	0.59	8.0	42	3
39.0227	3	LWWVWNNQSLPVSPRL	2326	CEA.177	217	1552	3049	1
39.0228	2	QYSWFVNGTFQQSTQ	2327	CEA.268	192	80	926	3
39.0229	2	DTGLNRTTVTTITVY	2328	CEA.305	--	--	2841	0
39.0230	2	KPFITSNNSNPVEDE	2329	CEA.324	--	--	--	0
39.0231	2	NRTLTLSSVTRNDVG	2330	CEA.375	238	--	--	1
39.0232	2	QELFISNITEKNSGL	2331	CEA.460	--	2500	--	0
39.0233	3	RTTVKTITVSAELPK	2332	CEA.488	455	7031	317	2
39.0234	2	SAELPKPSISSNNSK	2333	CEA.497	--	--	--	0
39.0235	2	LDVLYGPDTPHISPP	2334	CEA.587	--	--	--	0
39.0236	2	TQVLFIAKITPNNNG	2335	CEA.637	61	--	6579	1
39.0237	2	QVLFIAKITPNNNGT	2336	CEA.638	42	1875	--	1
39.0238	3	YACFVSNLATGRNNS	2337	CEA.653	208	1667	3571	1
39.0239	2	NNSIVKSITVSASGT	2338	CEA.665	91	25	676	3
39.0240	3	NSIVKSITVSASGTS	2339	CEA.666	78	25	329	3

-- indicates binding affinity =10,000nM.

added



Table XXX DR supertype crossbinding

Peptide	Sequence	SEQ ID NO:	Source	DR1 nM	DR4w4 nM	DR7 nM	DR2w2B1 nM	DR2w2B2 nM	DR6w19 nM	DR5w11 nM	DR8w2 nM	DR147 Degen	Broad Degen (5/8)
39.0217	RWCIPWQRLLLTASL	2340	CEA.10	8.2	542	357	827	--	318	--	--	3	5
39.0219	EVLVVHNLPHLFG	2341	CEA.50	2.0	52	53	40	--	1.0	588	408	3	7
39.0220	GREIYPNASLLIQN	2342	CEA.97	8.1	484	45	24	8333	2.9	6897	5904	3	5
39.0221	EIIYPNASLLIQNII	2343	CEA.99	14	1154	156	57	--	11	--	--	2	4
39.0223	DTGFYTLHVKSDEL	2344	CEA.116	69	1731	227	506	800	3889	2500	790	2	5
39.0226	YLWVNNQSLPVSPR	2345	CEA.176	0.60	8.0	42	110	2105	2.3	29	1065	3	6
39.0228	QYSWFVNGTFQQSTQ	2346	CEA.268	192	80	926	--	6061	5833	370	--	3	4
39.0233	RTTVKTITVSAELPK	2347	CEA.488	455	7031	317	364	--	700	--	--	2	4
39.0239	NNSIVKSITVSASGT	2348	CEA.665	91	25	676	3138	--	51	--	4083	3	4
39.0240	NSIVKSITVSASGTS	2349	CEA.666	78	25	329	3957	--	76	--	2882	3	4

-- indicates binding affinity = 10,000nM.



Table XXXI. DR3 binding

Peptide	Sequence	SEQ ID NO:	Source	DR3 nM
39.0313	QNIIQN DTGFYTLHV	2350	CEA.110	938
39.0314	LHVIKSDLVNEEATG	2351	CEA.122	2308
39.0315	KSDLVNEEATGQFRV	2352	CEA.126	--
39.0316	SDLVNEEATGQFRVY	2353	CEA.127	--
39.0317	NEEATGQFRVYPELP	2354	CEA.131	--
39.0318	QFRVYPELPKPSISS	2355	CEA.137	--
39.0319	AVAFTCEPETQDATY	2356	CEA.162	--
39.0320	TASYKCETQNPVSAR	2357	CEA.210	--
39.0321	NVLYGPDAPTISPLN	2358	CEA.232	--
39.0322	ISPLNTSYRSGENLN	2359	CEA.242	--
39.0323	SGSYTCQAHNSDTGL	2360	CEA.294	--
39.0324	TITVYAEPPKPFITS	2361	CEA.315	--
39.0325	SNPVEDEDAVALTCE	2362	CEA.332	--
39.0326	AVALTCEPEIQNTTY	2363	CEA.340	--
39.0327	NQSLPVSPRLQLSND	2364	CEA.360	--
39.0328	RLQLSNDNRTLTLIS	2365	CEA.368	938
39.0329	ECGIQNELSDHSDP	2366	CEA.392	--
39.0330	QNELSDHSDPVILN	2367	CEA.396	3659
39.0331	NVLYGPDDPTISPSY	2368	CEA.410	--
39.0332	GVNLSLSCHAASNPP	2369	CEA.430	--
39.0333	TITVSAELPKPSISS	2370	CEA.493	--
39.0334	AVAFTCEPEAQNTTY	2371	CEA.518	--
39.0335	SDPVTL DVLYGPDTP	2372	CEA.582	--
39.0336	DVLYGPDTPHISPPD	2373	CEA.588	--
39.0337	GANLNLSCHSASNPS	2374	CEA.608	--

-- indicates binding affinity =10,000nM.

Added



Table XXXII. HTL Candidate Epitopes

Peptide	Sequence	SEQ ID NO.	Motif	Source	DR1 nM	DR4w4 nM	DR7 nM	DR3 nM	DR2w2 β 1 nM	DR2w2 β 2 nM	DR6w1 9 nM	DR5w1 1 nM	DR8w2 nM	DR147 Cross-reactivity	Broad Cross-reactivity (5/8)	DR3 Binder
39.0217	RWCIPWQRLLLTASL	2375	DR sup	CEA.10	8.2	542	357	--	827	--	318	--	--	3	5	0
39.0219	EVLVVHNLPHLFG	2376	DR sup	CEA.50	2.0	52	53	336	40	--	1.0	588	408	3	7	1
39.0220	GREIYPNASLLIQN	2377	DR sup	CEA.97	8.1	484	45	1123	24	8333	2.9	6897	5904	3	5	0
39.0313	QNIQNDTGFTLHV	2378	DR3	CEA.110	1136	>8182	--	938	867	--	9.7	--	--	0	2	1
39.0223	DTGFYTLHVIKSDLV	2379	DR sup	CEA.116	69	1731	227	--	506	800	3889	2500	790	2	5	0
39.0226	YLWWVNNQSLPVSPR	2380	DR sup	CEA.176	0.60	8.0	42	2310	110	2105	2.3	29	1065	3	6	0
39.0328	RLQLSNDNRTLTLIS	2381	DR3	CEA.368	--	>8182	--	938	--	--	729	--	--	0	1	1

-- indicates binding affinity = 10,000nM

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